



# results of BLAST

## BLASTP 2.2.6 [Apr-09-2003]

### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1050528130-021341-18840

### Query=

(533 letters)

**Database:** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF

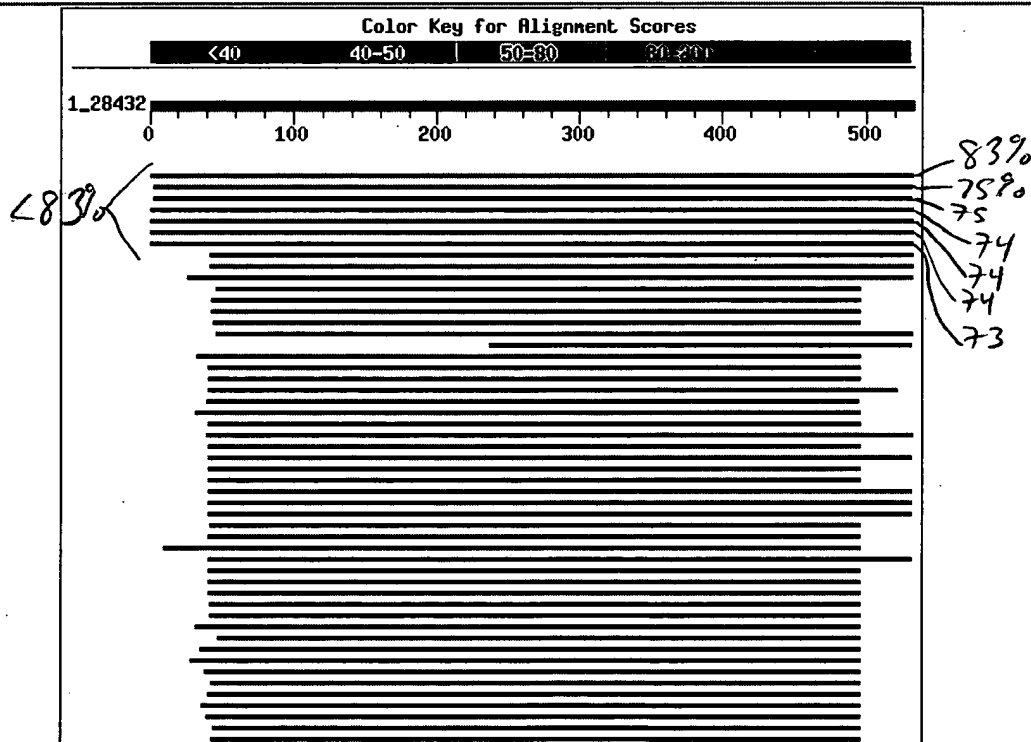
1,421,989 sequences; 457,202,972 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

## Distribution of 110 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Score E

## Sequences producing significant alignments:

(bits) Value

gi	5771354	dbj	BAA83501.1	Sucrose Transporter [Zea mays]	838	0.0
gi	9624451	gb	AAF90181.1	AF280050 1 sucrose transporter [Or...	758	0.0
gi	7489560	pir	T02982	probable sucrose transport protein -...	753	0.0
gi	20152871	gb	AAM13408.1	AF408842 1 sucrose transporter SU...	752	0.0
gi	7024415	emb	CAB75882.1	sucrose transporter 1 [Hordeum v...	751	0.0
gi	20152873	gb	AAM13409.1	AF408843 1 sucrose transporter SU...	749	0.0
gi	19548165	gb	AAL90455.1	AF408845 1 sucrose transporter SU...	747	0.0
gi	16152148	gb	AAL14982.1	AF419298 1 sucrose transporter [O...	586	e-166
gi	15718401	dbj	BAB68368.1	sucrose transporter [Oryza sati...	586	e-166
gi	21063927	gb	AAM29153.1	sucrose transporter 2 [Citrus si...	526	e-148
gi	29467454	dbj	BAC67164.1	sucrose transporter [Oryza sati...	526	e-148
gi	10119908	gb	AAG12987.1	AF166498 1 sucrose transporter-li...	525	e-148
gi	15227049	ref	NP_178389.1	putative sucrose/H+ symporter;...	523	e-147
gi	6434831	gb	AAF08330.1	AF021809 1 putative sucrose transp...	517	e-145
gi	29467456	dbj	BAC67165.1	sucrose transporter [Oryza sati...	502	e-141
gi	19071641	gb	AAL84308.1	AC073556 25 sucrose transporter, ...	416	e-115
gi	542020	pir	S43142	sucrose transport protein - castor be...	385	e-105
gi	4091891	gb	AAC99332.1	sucrose transporter [Apium graveo...	369	e-101
gi	15217601	ref	NP_177333.1	sucrose transport protein SUC1...	369	e-101
gi	5566434	gb	AAD45390.1	AF167415 1 sucrose transporter SUT...	367	e-100
gi	28172870	emb	CAD61275.1	sucrose transporter 4 protein [...	365	1e-99
gi	5882292	gb	AAD55269.1	AF182445 1 sucrose transporter [Vi...	364	2e-99
gi	15239949	ref	NP_196235.1	sucrose transporter protein; p...	364	2e-99
gi	1086253	pir	S38657	sucrose transport protein ptp1 - com...	364	2e-99
gi	18091779	gb	AAL58071.1	sucrose transporter SUC1 [Brassi...	364	2e-99
gi	5230818	gb	AAD41024.1	sucrose transport protein SUT1 [P...	363	4e-99
gi	15219938	ref	NP_173685.1	putative sucrose transport pro...	363	4e-99
gi	481131	pir	S38196	sucrose transport protein SUC2 - Arab...	363	4e-99
gi	7488866	pir	T12198	sucrose transport protein - fava bea...	363	5e-99
gi	7488936	pir	T14340	sucrose-proton transport protein - c...	363	6e-99
gi	7488935	pir	T14339	sucrose-proton transport protein - c...	362	6e-99
gi	6705993	dbj	BAA89458.1	sucrose transporter protein [Dau...	362	7e-99
gi	15219686	ref	NP_176830.1	sucrose-proton symporter, puta...	362	9e-99
gi	15217602	ref	NP_177334.1	putative sucrose transport pro...	362	1e-98
gi	12057172	emb	CAC19851.1	sucrose transporter [Arabidopsis...	361	1e-98
gi	20147213	gb	AAM10322.1	Atlg22710/T22J18_12 [Arabidopsis...	361	2e-98
gi	12038843	emb	CAC19689.1	sucrose/proton symporter [Daucu...	361	2e-98
gi	18091781	gb	AAL58072.1	sucrose transporter SUC2 [Brassi...	359	5e-98
gi	9957218	gb	AAG09270.1	AF176950 1 sucrose transporter [Ly...	359	6e-98
gi	10998390	gb	AAG25923.1	sucrose transporter SUT4 [Solanu...	358	9e-98
gi	6434829	gb	AAF08329.1	AF021808 1 putative sucrose transp...	358	2e-97
gi	9957053	gb	AAG09191.1	AF175321 1 sucrose transporter SUT...	356	6e-97
gi	15225986	ref	NP_179074.1	putative sucrose-proton sympor...	355	8e-97
gi	15218362	ref	NP_172467.1	putative sucrose/H+ symporter;...	355	1e-96
gi	542087	pir	JQ2389	sucrose transport protein - potato >g...	355	1e-96
gi	7649151	gb	AAF65765.1	AF242307 1 sucrose transport prote...	352	9e-96
gi	6434833	gb	AAF08331.1	AF021810 1 putative sucrose transp...	350	3e-95
gi	15239921	ref	NP_199174.1	sucrose transporter protein; p...	350	3e-95
gi	549000	sp	Q03411	STP SPIOL Sucrose transport protein (Su...	348	1e-94
gi	1076644	pir	S48789	sucrose transport protein - common t...	347	2e-94
gi	5823000	gb	AAD53000.1	U64967 1 sucrose-proton symporter ...	346	6e-94
gi	17447420	gb	AAF04295.2	AF191025 1 sucrose transporter 1 ...	345	8e-94
gi	6120115	gb	AAF04294.1	AF191024 1 sucrose transporter 1 [...	345	1e-93
gi	21063921	gb	AAM29150.1	citrus sucrose transporter 1 [Ci...	345	1e-93
gi	1086250	pir	S52377	sucrose transport protein SUC1 - com...	342	1e-92
gi	1076257	pir	S51114	sucrose-proton symporter - beet >gi ...	340	5e-92
gi	7024413	emb	CAB75881.1	sucrose transporter 2 [Hordeum v...	338	1e-91
gi	29467452	dbj	BAC67163.1	sucrose transporter [Oryza sati...	337	4e-91
gi	15217323	gb	AAK92667.1	AC090487 9 Putative sucrose trans...	318	2e-85
gi	25344709	pir	A86234	hypothetical protein [imported] - A...	315	1e-84
gi	575299	emb	CAA57726.1	sucrose transporter [Lycopersicon...	296	7e-79
gi	1076602	pir	S48788	sucrose transport protein - tomato (...	295	1e-78
gi	2980887	emb	CAA12256.1	Sucrose carrier [Ricinus communis]	295	1e-78



PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	MIM	Books	
Search		Protein	for					Go	Clear
		Limits	Preview/Index	History	Clipboard		Details		
Display	default	Show:	20	Send to	File	Get Subsequence			

☐ 1: BAA83501. Sucrose Transport...[gi:5771354]

[BLink](#), [Domains](#), [Links](#)

LOCUS BAA83501 521 aa linear PLN 26-AUG-1999  
 DEFINITION Sucrose Transporter [Zea mays].  
 ACCESSION BAA83501  
 VERSION BAA83501.1 GI:5771354  
 DBSOURCE accession [AB008464.1](#)  
 KEYWORDS .

SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (sites)  
 AUTHORS Aoki,N., Hirose,T., Takahashi,S., Ono,K., Ishimaru,K. and Ohsugi,R.  
 TITLE Molecular cloning and expression analysis of a gene for a sucrose  
 transporter in maize (Zea mays L.)

JOURNAL Plant Cell Physiol. (1999) In press

REFERENCE 2 (residues 1 to 521)

AUTHORS Aoki,N.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-OCT-1997) Naohiro Aoki, Japan International Research  
 Center for Agricultural Sciences, Biological Resources Division;  
 1-2 Ohwashi, Tsukuba, Ibaraki 305, Japan  
 (E-mail:naoki@ss.jircas.affrc.go.jp, Tel:81-0298-38-6305,  
 Fax:81-0298-38-6650)

FEATURES Location/Qualifiers  
 source 1..521  
 /organism="Zea mays"  
 /db\_xref="taxon:4577"  
 Protein 1..521  
 /product="Sucrose Transporter"  
 CDS 1..521  
 /gene="ZmSUT1"  
 /coded\_by="AB008464.1:168..1733"

#### ORIGIN

```

1 margdgelel svgvrgtgga aaaaaadhva pislgrlila gmvaggvqyg walqlsl1tp
61 yvqtlglsha ltsfmwlcgp iaglvvqplv glysdrcstar wgrrrpfili gcmliclavi
121 vvgfssdiga algtkkehcs lyhgprwhaa ivyvlgfll dfsnntvqgp arammadlcg
181 hhgpsaansi fcswmalgni lgyssgstnn whkwfpfllt nacceacanl kgaf1vavvf
241 lvmcltvtlf fanevpyrgn qnlptkange vetepsgpla vlkgfkn1pt gmpsvllvtg
301 ltwlswfpfi lydtldwmgre iyhgdpkgsn aqisafdegv rvgsfgllln sivlgfssfl
361 iepmcrkvqp rvwvtsnfm vcvamaatal isfws1kdyh gyvqdaitas tsikavclvl
421 faflgvplai lysvpfavta qlaatkgggq glctgvlnis ivipqviial gagpwdalfg
481 kgnipafgva sgfaliggvv gvfillpkisk rqfravsagg h

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gi	4960089	gb	AAD34610.1	AF149981.1	sucrose transporter-lik...	294	2e-78	
gi	16930709	gb	AAL32020.1		sucrose transporter [Vitis vinif...	277	2e-73	
gi	13186184	emb	CAC33492.1		sucrose carrier [Ricinus communis]	269	8e-71	
gi	14161680	gb	AAK54856.1		sucrose transporter [Oryza sativa]	241	2e-62	
gi	14161682	gb	AAK54857.1		sucrose transporter [Oryza sativa]	239	6e-62	
gi	27227722	emb	CAD29832.1		sucrose transporter [Viscum alb...	222	1e-56	
gi	17402525	dbj	BAB78696.1		sucrose transporter [Nicotiana ...]	220	4e-56	
gi	28830172	gb	AAO52628.1		similar to Arabidopsis thaliana ...	211	3e-53	
gi	5640023	gb	AAD45932.1	AF168771.1	sucrose transport prote...	211	3e-53	
gi	28371870	gb	AAO38059.1		sucrose transporter SUC1 [Brassi...	177	3e-43	
gi	28143940	gb	AAO26335.1		putative sucrose transporter [Br...	159	2e-37	
gi	27447671	gb	AAO13696.1		sucrose transporter [Lycopersico...	137	4e-31	
gi	26522780	dbj	BAC44864.1		hypothetical protein [Glycine max]	110	5e-23	
gi	11596257	gb	AAG38546.1	AF309805.1	putative sucrose carr...	102	2e-20	
gi	28917846	gb	EAA27533.1		hypothetical protein [Neurospora...	100	7e-20	
gi	19115299	ref	NP_594387.1		putative sucrose carrier [Schi...	99	1e-19	
gi	21426811	ref	NP_653348.1		proton-associated sugar transp...	99	2e-19	<a href="#">L</a>
gi	16716355	ref	NP_444307.1		membrane associated transporte...	98	3e-19	<a href="#">L</a>
gi	21293355	gb	EAA05500.1		agCP10413 [Anopheles gambiae str...	98	4e-19	
gi	17369709	sp	Q9UMX9	MATP HUMAN	Membrane-associated transp...	97	5e-19	<a href="#">L</a>
gi	26354753	dbj	BAC41003.1		unnamed protein product [Mus mu...	97	5e-19	<a href="#">L</a>
gi	28872809	ref	NP_057264.2		membrane-associated transporte...	97	5e-19	<a href="#">L</a>
gi	15004313	gb	AAK77024.1	AF332510.1	membrane-associated tr...	97	6e-19	
gi	27688281	ref	XP_226834.1		similar to membrane associated...	97	7e-19	<a href="#">L</a>
gi	27719225	ref	XP_235397.1		similar to KIAA1126 protein [H...	95	3e-18	<a href="#">L</a>
gi	13097810	gb	AAH03597.1	AAH03597	Similar to AIM-1 protein...	92	2e-17	<a href="#">L</a>
gi	27948583	gb	AAO25647.1		membrane-associated transporter ...	92	2e-17	
gi	21244213	ref	NP_643795.1		sugar transporter [Xanthomonas...	92	2e-17	
gi	24661424	ref	NP_648292.1		CG4484-PA [Drosophila melanoga...	91	4e-17	<a href="#">L</a>
gi	21232786	ref	NP_638703.1		sugar transporter [Xanthomonas...	89	1e-16	
gi	6651341	gb	AAF22281.1	AF167417.1	putative sucrose transp...	88	4e-16	
gi	22122421	ref	NP_666089.1		hypothetical protein MGC32471 ...	85	3e-15	<a href="#">L</a>
gi	27712020	ref	XP_222629.1		similar to hypothetical protei...	84	4e-15	<a href="#">L</a>
gi	14916437	ref	NP_149093.1		prostein protein [Homo sapiens...	83	1e-14	<a href="#">L</a>
gi	21294249	gb	EAA06394.1		ebiP8133 [Anopheles gambiae str....]	81	3e-14	
gi	13874497	dbj	BAB46871.1		hypothetical protein [Macaca fa...	81	4e-14	
gi	6473156	dbj	BAA87101.1		Hypothetical protein [Schizosacc...	79	1e-13	

## Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|5771354|dbj|BAA83501.1| Sucrose Transporter [Zea mays]  
Length = 521

Score = 838 bits (2166), Expect = 0.0

Identities = 447/538 (83%), Positives = 461/538 (85%), Gaps = 22/538 (4%)

Query: 1 MARGDGGQLAELSAGVRGAAA-----VVDHVAPISLGRILLAGMVAPISLGRILLAGMVA 55  
MARGDG ELS GVRG DHVAPISLG RLILAGMVA  
Sbjct: 1 MARGDGE--LELSVGVRGTGGAAAAAADHVAPISLG-----RLILAGMVA 44

Query: 56 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCPGPIAGLVVQPLVGLYSDRCTSRWGRR 115  
GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCPGPIAGLVVQPLVGLYSDRCT+RWGRR  
Sbjct: 45 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCPGPIAGLVVQPLVGLYSDRCTARWGRR 104

Query: 116 RPFILTGCMILICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFSN 175  
RPFIL GCMILIC+AVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFSN  
Sbjct: 105 RPFILIGCMILICLAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFSN 164

Query: 176 NTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPLKTSACC 235

NTVQGPARAMMADLC HHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFL T+ACC  
 Sbjct: 165 NTVQGPARAMMADLCGHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLTNACC 224

Query: 236 EACANLKGXXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLK 295  
 EACANLKG FA EVPYR N+NLP TKA GEVETEP+GPLAVLK  
 Sbjct: 225 EACANLKGAFVLAVVFLVMCLTTLFFANEVPGRNQNLN- TKANGEVETEPSGPLAVLK 283

Query: 296 GFKDLPPGMPVSVLLVTAITWLSWFPFILIYD TDWMDGREIYHGD PKGSNAQISAFNEGVRVG 355  
 GFK+LP GMPVSVLLVT +TWLSWFPFILIYD TDWMDGREIYHGD PKGSNAQISAF+EGVRVG  
 Sbjct: 284 GFKNLPTGMPVSVLLVTGLTWLSWFPFILIYD TDWMDGREIYHGD PKGSNAQISAFDEGVRVG 343

Query: 356 AFGLLLNSVILGFSSFLIEPMCRKVGPVVVWTSNFMVCVAMAATALISFWSLRDYGHYV 415  
 +FGLLLS++LGFSSFLIEPMCRKVGPVVVWTSNFMVCVAMAATALISFWSL+DYGHYV  
 Sbjct: 344 SFGLLLNSIVLGFSSFLIEPMCRKVGPVVVWTSNFMVCVAMAATALISFWSLKDYHGYY 403

Query: 416 QDAITANASIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVI 475  
 QDAITA+ SIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAAT+GGGQGLCTGVLNISIVI  
 Sbjct: 404 QDAITASTSIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATKGGGQGLCTGVLNISIVI 463

Query: 476 PQVIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533  
 PQVIALGAGPWDALFGKGNIP PKISKRQFRAVSAGGH  
 Sbjct: 464 PQVIALGAGPWDALFGKGNIPAFGVASGFALIGGVGVFLLPKISKRQFRAVSAGGH 521

☐ >gi|9624451|gb|AAF90181.1|AF280050 1 sucrose transporter [Oryza sativa (indica c  
 Length = 538

Score = 758 bits (1958), Expect = 0.0

Identities = 399/529 (75%), Positives = 432/529 (81%), Gaps = 4/529 (0%)

Query: 4 GDGGQLAELSAGVRGAAAVVDHVAPISLGRILLAGMVAPISLGRILLAGMVAGGVQYGWA 63  
 G GG ELS G APISLGRILLAGMVAGGVQYGWA  
 Sbjct: 12 GGGGGGLELS---VGVGGGGGARGGGGGEAAAAVETAAPISLGRILLAGMVAGGVQYGWA 68

Query: 64 LQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLYSDRCTSRWGRRRPFILTGC 123  
 LQLSLLTPYVQTLGLSHALTSFMWLCGPIAG+VVQP VGLYSDRCTS+WGRRRP+ILTGC  
 Sbjct: 69 LQLSLLTPYVQTLGLSHALTSFMWLCGPIAGMVVQPCVGLYSDRCTSKWGRRRPPYILTGC 128

Query: 124 MLICVAVIVVGFS DIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFSNNTVQGP 183  
 +LIC+AV+V+GFS+DIG A+GDTKE CS+YHG RWHAAIVYVLGFWLLDFSNNTVQGP  
 Sbjct: 129 VLICLAVVIGFSADIGYAMGDTKEDCSVYHGSRWHAAIVYVLGFWLLDFSNNTVQGP 188

Query: 184 AMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLKTSACCEACANLKG 243  
 A+MADL HGP ANSIFCSWMA+GNILGYSSGSTNNWHKWFPFLKT ACCEACANLKG  
 Sbjct: 189 ALMADLSGRHGP GTANSIFCSWMAMGNILGYSSGSTNNWHKWFPFLKTRACCEACANLKG 248

Query: 244 XXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLKGFKDLPPG 303  
 IFAKEVP++ N LP TK+ E E TGPLAVLKGF++LP G  
 Sbjct: 249 AFLVAVIFLSLCLVITLIFAKEVPFKGNAALP-TKSNEPAEPEGTGPLAVLKGFRLNPTG 307

Query: 304 MPSVLLVTAITWLSWFPFILIYD TDWMDGREIYHGD PKGSNAQISAFNEGVRVGAFGLLLNS 363  
 MPSVL+VT +TWLSWFPFILIYD TDWMDGREIYHGD PKG++ QI AFN+GVR GAFGLLLNS  
 Sbjct: 308 MPSVLIVTGLTWLSWFPFILIYD TDWMDGREIYHGD PKGTDPQIEAFNQGVRA GAFGLLLNS 367

Query: 364 VILGFSSFLIEPMCRKVGPVVVWTSNFMVCVAMAATALISFWSLRDYGHYVQDAITANA 423  
 ++LGFSSFLIEPMCRKVGPVVVWTSNFMVCVAMAATALISFWSL+D+HG VQ AITA+  
 Sbjct: 368 IVLGFSSFLIEPMCRKVGPVVVWTSNFMVCVAMAATALISFWSLKDFHGT VQKAITADK 427

Query: 424 SIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVIALG 483  
 SIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQV+IALG  
 Sbjct: 428 SIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVIALG 487

Query: 484 AGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGG 532  
 AGPWD LFGKGNIP PKISKRQFR+VS GG  
 Sbjct: 488 AGPWDELFGKGNIPAFGLASGFALIGGVAGIFLLPKISKRQFRSVSMGG 536

☐ >gi|7489560|pir|T02982 probable sucrose transport protein - rice  
gi|2723471|dbj|BAA24071.1| sucrose transporter [Oryza sativa (japonica cultivar-g  
Length = 537

Score = 753 bits (1944), Expect = 0.0

Identities = 397/529 (75%), Positives = 430/529 (81%), Gaps = 5/529 (0%)

Query: 4 GDGGQLAELSAGVRGAAAVVDHVAPISLGRILLAGMVAPISLGRILLAGMVAGGVQYGWA 63  
G GG ELS APISLGRILLAGMVAGGVQYGWA  
Sbjct: 12 GGGGGGLELS----VGVGGGGARGGGGGEAAAETAAPISLGRILLAGMVAGGVQYGWA 67

Query: 64 LQLSLLTPYVQTLGLSHALTSFMWLCGPVAGLVVQPLVGLYSDRCTSRWGRRRPFILTC 123  
LQLSLLTPYVQTLGLSHALTSFMWLCGPVAGLVVQPLVGLYSDRCTSRWGRRRPFILTC  
Sbjct: 68 LQLSLLTPYVQTLGLSHALTSFMWLCGPVAGLVVQPLVGLYSDRCTSKWGRRRPFILTC 127

Query: 124 MLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFLLDFSNNTVQGP 183  
+LIC+AV+V+GFS+DIG A+GDTKE CS+YHG RWHAAIVYVLGFLLDFSNNTVQGP  
Sbjct: 128 VLICLAVVIGFSADIGYAMGDTKEDCSVYHGSRWHAAIVYVLGFLLDFSNNTVQGP 187

Query: 184 AMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLKTSACCEACANLKG 243  
A+MADL HGP ANSIFCSWMA+GNILGYSSGSTNNWHKWFPFLKT ACCEACANLKG  
Sbjct: 188 ALMADLSGRHGPGTANSIFCSWMAMGNILGYSSGSTNNWHKWFPFLKTRACCEACANLKG 247

Query: 244 XXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLKGFCDLPPG 303  
IFAKEVP++ N LP TK+ E E TGPLAVLKGF++LP G  
Sbjct: 248 AFLVAVIFLSLCLVITLIFAKEVPFKGNAALP-TKSNEPAEPEGTGPLAVLKGFRLNPTG 306

Query: 304 MPSVLLVTAITWLSWFPFILIYDTDWMGREIYHGD PKGSNAQISAFNEGVRVGAFLGLLNS 363  
MPSVL+VT +TWLSWFPFILIYDTDWMGREIYHGD PKG++ QI AFN+GVR GAFGLLNS  
Sbjct: 307 MPSVLIVTGLTWLSWFPFILIYDTDWMGREIYHGD PKGTDPIEAFNQVRAGAFGLLNS 366

Query: 364 VILGFSSFLIEPMCRKVGPRVWVTSNFMVCVAMAATALISFWSLRDYHGYVQDAITANA 423  
++LGFSSFLIEPMCRKVGPRVWVTSNF+VC+AMAATALISFWSL+D+HG VQ AITA+  
Sbjct: 367 IVLGFSSFLIEPMCRKVGPRVWVTSNFLVCIAAMAATALISFWSLKDFHGTQKAITADK 426

Query: 424 SIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVIALG 483  
SIKAVCLVLF AFLGVPLA+LYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQV+IALG  
Sbjct: 427 SIKAVCLVLF AFLGVPLAVLYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVIALG 486

Query: 484 AGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGG 532  
AGPWD LFGKNIP PKISKRQF +VS GG  
Sbjct: 487 AGPWDELFGKGNIPAFGLASGFALIGGVAGIFLLPKISKRQFWSVSMGG 535

☐ >gi|20152871|gb|AAM13408.1|AF408842.1 sucrose transporter SUT1A [Triticum aestiv  
Length = 522

Score = 752 bits (1941), Expect = 0.0

Identities = 398/533 (74%), Positives = 435/533 (81%), Gaps = 11/533 (2%)

Query: 1 MARGDGGQLAELSAGVRGAAAVVDHVAPISLGRILLAGMVAPISLGRILLAGMVAGGVQY 60  
MARG G ELS GV G A ++ ISLGRILLAGMVAGGVQY  
Sbjct: 1 MARGGGNGEVELSVGVGGGGAGAGGADAPAVD-----ISLGRILLAGMVAGGVQY 50

Query: 61 GWALQLSLLTPYVQTLGLSHALTSFMWLCGPVAGLVVQPLVGLYSDRCTSRWGRRRPFIL 120  
GWALQLSLLTPYVQTLGLSHALTSFMWLCGPVAGLVVQPLVGLYSD+CTSRWGRRRPFIL  
Sbjct: 51 GWALQLSLLTPYVQTLGLSHALTSFMWLCGPVAGLVVQPLVGLYSDKCTSRWGRRRPFIL 110

Query: 121 TGCMLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFLLDFSNNTVQGP 180  
TGC+LIC+AV+VVGFS+DIGAALGDTKE CSLYHGPRWHAAIVYVLGFLLDFSNNTVQGP  
Sbjct: 111 TGCILICIAVVVGFSSADIGALGDSKECSLYHGPRWHAAIVYVLGFLLDFSNNTVQGP 170

Query: 181 PARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLKTSACCEACAN 240  
PARA+MADL HGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFL+T ACCEACAN  
Sbjct: 171 PARALMADLSAQHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLRTRACCEACAN 230

Query: 241 LKGXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLP TTKAGGEVETEPTGPLAVLKGFKDL 300  
 LKG IFAKE+PY+A LP TKA G+VE EPTGPLAV KGFK+L  
 Sbjct: 231 LKGAFVLAVLFLAFCLVITVIFAKEIPYKAIAPLP-TKANGQVEVEPTGPLAVFKGFKNL 289

Query: 301 PPGMPSVLLVTAITWLSWFPFILIYD TDW MGREIYHGDPKGSNAQISAFNEGVRVGA FG LL 360  
 PPGMPSVLLVT +TWLSWFPFILIYD TDW MGREIYHGDPKG+ + +AF GVR GAFGLL  
 Sbjct: 290 PPGMPSVLLVTGLTWLSWFPFILIYD TDW MGREIYHGDPKGTPEANAFQAGVRAGAFGLL 349

Query: 361 LNSVILGFSSFLIEPMC RKVGPRVWVTSNFMVCVMAAATALISFWSLRDYHGYVQDAIT 420  
 LNSV+LGFSSFLIEP+C+++GPRVWV+SNF+VC++MAA +IS+W+ +D HGY+Q AIT  
 Sbjct: 350 LNSVILGFSSFLIEPLCKRLGPRVWVSSNFLVCLSMACIISWWATQDLHGYIQHAIT 409

Query: 421 ANASIKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVII 480  
 A+ IK V L LFAFLG+PLAILYSVPFAVTAQLAA RGGGQGLCTGVLNI+IVIPQVII  
 Sbjct: 410 ASKEIKIVSLALFAFLGIPLAILYSVPFAVTAQLAANRGGGQGLCTGVLNIAIVIPQVII 469

Query: 481 ALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533  
 A+GAGPWD LFGKGNIP PKIS+RQFRAVS GGH  
 Sbjct: 470 AVGAGPWDELFGKGNIPAFGVASAFALIGGIVGIFLLPKISRRQFRAVSGGGH 522

☐ >gi|7024415|emb|CAB75882.1| sucrose transporter 1 [Hordeum vulgare subsp. vulgar]  
 Length = 523

Score = 751 bits (1939), Expect = 0.0  
 Identities = 399/538 (74%), Positives = 434/538 (80%), Gaps = 20/538 (3%)

Query: 1 MARGDGGQLAELS-----AGVRGAAAVVDHVAPISLGRLLLAGMVAPISLGRLLLAGMVA 55  
 MARG G ELS G A + ISLG RLILAGMVA  
 Sbjct: 1 MARGGNGEVELSVGVGGGGGGAAPRAEPAVQISLG-----RLILAGMVA 46

Query: 56 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLYSDRCTSRWGRR 115  
 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQP VGLYSD+CTSRWGRR  
 Sbjct: 47 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRR 106

Query: 116 RPFILTGCM LICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVVVLGFWLLDFSN 175  
 RPFILTG C+LIC+AVI+VGFS+DIGAALGD+KE CSLYHGPRWHAAIVVVLGFWLLDFSN  
 Sbjct: 107 RPFILTGCVLICLA V IIVGFSADIGAALGDSKEECSLYHGPRWHAAIVVVLGFWLLDFSN 166

Query: 176 NTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLKTSACC 235  
 NTVQGPARA+MADL HGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFL+T ACC  
 Sbjct: 167 NTVQGPARAMMADLSAQHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLRTRACC 226

Query: 236 EACANLKGXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLP TTKAGGEVETEPTGPLAVLK 295  
 EACANLKG IFAKEVPY+A LP TKA G+VE EPTGPLAV K  
 Sbjct: 227 EACANLKGAFVLAVLFLSLALVITLIFAKEVPYKAIAPLP-TKANGQVEVEPTGPLAVFK 285

Query: 296 GFKDLPPGMPSVLLVTAITWLSWFPFILIYD TDW MGREIYHGDPKGSNAQISAFNEGVRVG 355  
 GFK+LPPGMPSVLLVT +TWLSWFPFILIYD TDW MGREIYHGDPKG+ A+ +AF EGVR G  
 Sbjct: 286 GFKNLPPGMPSVLLVTGLTWLSWFPFILIYD TDW MGREIYHGDPKGTPEANAFQEGVRAG 345

Query: 356 AFGLLLNSVILGFSSFLIEPMC RKVGPRVWVTSNFMVCVMAAATALISFWSLRDYHGYV 415  
 AFGLLLNSV+LGFSSFLIEPMC+++GPRVWV+SN +VC++MAA +IS+W+ +D HGY+  
 Sbjct: 346 AFGLLLNSVILGFSSFLIEPMCRLGPRVWVSSNMLVCLSMACIISWWATQDLHGYI 405

Query: 416 QDAITANASIKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVI 475  
 Q AITA+ IKAV L LFAFLG+PLAILYSVPFAVTAQLAA +GGGQGLCTGVLNI+IVI  
 Sbjct: 406 QHAITASKEIKAVSLALFAFLGIPLAILYSVPFAVTAQLAANKGGGQGLCTGVLNIAIVI 465

Query: 476 PQVIIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533  
 PQVIIA+GAGPWD LFGKGNIP PKIS+RQFRAVS GGH  
 Sbjct: 466 PQVIIAVGAGPWDELFGKGNIPAFGMASVFALIGGVVIGIFLLPKISRRQFRAVSGGGH 523

☐ >gi|20152873|gb|AAM13409.1|AF408843 1 sucrose transporter SUT1B [Triticum aestiv]  
 Length = 522

Score = 749 bits (1934), Expect = 0.0

Identities = 398/533 (74%), Positives = 434/533 (81%), Gaps = 11/533 (2%)

Query: 1 MARGDGGQLAELSAGVRGAAAVVDHVAPISLGRILLAGMVAPISLGRILLAGMVAGGVQY 60  
 MARG G ELS GV G A ++ ISLGRILLAGMVAGGVQY  
 Sbjct: 1 MARGGGNGEVELSVGVGGGGAGAGGADAPAVD-----ISLGRILLAGMVAGGVQY 50

Query: 61 GWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLYSDRCTSRWGRRRPFIL 120  
 GWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQP VGLYSD+CTSRWGRRRPFIL  
 Sbjct: 51 GWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRRRPFIL 110

Query: 121 TGCMLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFSNNTVQG 180  
 TG +LIC+AV+VVGFS+DIGAALGD+KE CSLYHGPRWHAAIVYVLGFWLLDFSNNTVQG  
 Sbjct: 111 TGYILICIAVVVVGFSADIGAALGDSKEECSLYHGPRWHAAIVYVLGFWLLDFSNNTVQG 170

Query: 181 PARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLKTSACCEACAN 240  
 PARA+MADL HGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFL+T ACCEACAN  
 Sbjct: 171 PARALMADLSAQHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLRTRACCEACAN 230

Query: 241 LKGXXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLKGFKDL 300  
 LKG IFAKE+PY+A LP TKA G+VE EPTGPLAV KGFK+L  
 Sbjct: 231 LKGAFLVAVLFLAFCLVITVIFAKEIPYKAIAPLP-TKANGQVEVEPTGPLAVFKGFKNL 289

Query: 301 PPGMPSVLLVTAITWLSWFFILYDTDWMGREIYHGD PKGSNAQISAFNEGVRVGAFLGL 360  
 PPGMPSVLLVT +TWLSWFFILYDTDWMGREIYHGD PKG+ + +AF GVR GAFLGL  
 Sbjct: 290 PPGMPSVLLVTGLTWLSWFFILYDTDWMGREIYHGD PKGTPDEANAFQAGVRAGAFGLL 349

Query: 361 LNSVILGFSSFLIEPMC RKVGRPVVWVTSNFMVCVAMAATALISFWSLRDYG YVQDAIT 420  
 LNSV+LGFSSFLIEP+C+++GPRVVWV+SNF+VC++MAA +IS+W+ +D HGY+Q AIT  
 Sbjct: 350 LNSVILGFSSFLIEPLCKRLGPRVVWVSSNFLVCLSMACIISWWATQDMHGYIQHAIT 409

Query: 421 ANASIKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVII 480  
 A+ IK V L LFAFLGVPLAILYSVPFAVTAQLAA RGGGQGLCTGVLNI+IVIPQVII  
 Sbjct: 410 ASKEIKIVSLALFAFLGVPLAILYSVPFAVTAQLAANRGGGQGLCTGVLNIAIVIPQVII 469

Query: 481 ALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533  
 A+GAGPWD LFGKGNIP PKIS+RQFRAVS GGH  
 Sbjct: 470 AVGAGPWDELFGKGNIPAFGMASAFALIGGIVGIFLLPKISRRQFRAVSGGGH 522

☐ >gi|19548165|gb|AAL90455.1|AF408845 1 sucrose transporter SUT1D [Triticum aestiv  
 gi|20152875|gb|AAM13410.1|AF408844 1 sucrose transporter SUT1D [Triticum aestivum  
 Length = 523

Score = 747 bits (1928), Expect = 0.0

Identities = 397/538 (73%), Positives = 432/538 (80%), Gaps = 20/538 (3%)

Query: 1 MARGDGGQLAELSAGVRGAAAVVDH-----VAPISLGRILLAGMVAPISLGRILLAGMVA 55  
 MARG G ELS GV G ISLG RLILLAGMVA  
 Sbjct: 1 MARGGGNGEVELSVGVGGGGGAAGGGEQPAVDISLG-----RLILLAGMVA 46

Query: 56 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLYSDRCTSRWGRR 115  
 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQP VGLYSD+CTSRWGRR  
 Sbjct: 47 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRR 106

Query: 116 RPFILTGCMILICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFS 175  
 RPFILTG+C+LIC+AV+VVGFS+DIGAALGD+KE CSLYHGPRWHAAIVYVLGFWLLDFS  
 Sbjct: 107 RPFILTGILICIAVVVVGFSADIGAALGDSKEECSLYHGPRWHAAIVYVLGFWLLDFS 166

Query: 176 NTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLKTSACC 235  
 NTVQGPARA+MADL HGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFL+T ACC  
 Sbjct: 167 NTVQGPALMADLSAQHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLRTRACC 226

Query: 236 EACANLKGXXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLK 295  
 EACANLKG IFAKE+PY+A LP TKA G+VE EPTGPLAV K  
 Sbjct: 227 EACANLKGAFVAVLFLAFCLVITVIFAKEIPYKAIAPLP-TKANGQVEVEPTGPLAVFK 285



Query: 296 GFKDLPPGMPSVLLVTAITWLSWFFILYD TDWMGREIYHGD PKGSNAQISAFNEGVRVG 355  
 GFK+LPPGMPSVLLVT +TWLSWFFILYD TDWMGREIYHGD PKG+ +AF GVR G  
 Sbjct: 286 GFKNLPPGMPSVLLVTGLTWLSWFFILYD TDWMGREIYHGD PKGTPDEANAFQAGVRAG 345

Query: 356 AFGLLLNSVILGFSSFLIEPMCRKVGPRVWVTSNFMVCVAMAATALISFWSLRDYG YV 415  
 AFGLLLNSV+LGFSSFLIEP+C+++GPRVWV+SNF+VC++MAA +IS+W+ +D HGY+  
 Sbjct: 346 AFGLLLNSVILGFSSFLIEPLCKRLGPRVWVSSNFLVCLSMACIISWATQDLHG YI 405

Query: 416 QDAITANASIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRG GGGQGLCTGVLNISI VI 475  
 Q AITA+ IK V L LFAFLG+PLAILYSVPFAVTAQLAA RGGGQGLCTGVLNI+IVI  
 Sbjct: 406 QHAITASKEIKIVSLALFAFLGIPLAILYSVPFAVTAQLAAKRGGGQGLCTGVLNIAIVI 465

Query: 476 PQVIIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533  
 PQVIAA+GAGPWD LFGKGNIP PKIS+RQFRAVS GGH  
 Sbjct: 466 PQVIIAVGAGPWDELFGKGNIPAFGMASAFALIGGIVGIFLLPKISRRQFRAVSGGGH 523

☐ >gi|16152148|gb|AAL14982.1|AF419298.1 sucrose transporter [Oryza sativa (indica  
 Length = 506

Score = 586 bits (1511), Expect = e-166  
 Identities = 330/494 (66%), Positives = 375/494 (75%), Gaps = 11/494 (2%)

Query: 43 ISLGRILLAGMVAGGVQYGWALQSLSLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVG 102  
 ISL L LA MVAGGVQYGWALQSLSLTPY+QTLG+ HALTS MWLCGPIAGL+VQP VG  
 Sbjct: 21 ISLSGLFLACMVAGGVQYGWALQSLSLTPYIQTGLIPHALTSVMWLCGPIAGLIVQPCVG 80

Query: 103 LYSDRCTSRWGRRRPFILTGCM LICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHA AI 162  
 LYSD+CTS GRRRPFILTG++IC++VIV+GFSSDIG ALGD E C +Y GPR+HAA  
 Sbjct: 81 LYSDKCTSSLGRRRPFILTGCIICISVIVIGFSSDIGYALGDATEDCKVYRGPRYHAAA 140

Query: 163 VYVLGFWLLDFSNNTVQGPARAMADL CDH HGPSAANSIFCSWMALGNILGYSSGSTNNW 222  
 ++LGFWLLDFSNNTVQGPARA+MADL HGPSAAN+IFCSWMALGNILGYSSGSTN+W  
 Sbjct: 141 AFILGFWLLDFSNNTVQGPALMADLSGRHGPSAANAIFCSWMALGNILGYSSGSTNDW 200

Query: 223 HKWFPFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGE 282  
 HKWFPFL T ACCEACANLK +FA+EV L A  
 Sbjct: 201 HKWFPFLMTRACCEACANLKA AFLVAVVFLGLSTAVTMVFAREVA-----LDPVAAAKR 254

Query: 283 VETEPTGPLAVLKGFKDLPPGMPSVLLVTAITWLSWFFILYD TDWMGREIYHGD PKGSN 342  
 E E +GPLAV KG K+LP GMPSVL+VT +TWLSWFFIL+DTDWMGREIYHG P GS  
 Sbjct: 255 NEGEASGPLAVFKGMKNLPVGMPSVLIVTGLTWLSWFFILFD TDWMGREIYHGRPDGSP 314

Query: 343 AQISAFNEGVRVGAFGLLLNSVILGFSSFLIEPMCRKVGPRVWVTSNFMVCVAMAATAL 402  
 A+++AF EGVR GAFGLLLNS++LG SSFLIEPMCR++G R VWV S+ +VCVAMAA ++  
 Sbjct: 315 AEVTAFAQEGVRQGAFLGLLLNSIVLGISSFLIEPMCRRLGARAVWVMSSAVVCVAMAAVSV 374

Query: 403 ISFWSLRDYG YVQDAITANAS---IKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRG 459  
 +S WSL D+ G VQDA A A ++A L LF FLG+P A+L SVPFAVTAQL A+RG  
 Sbjct: 375 LSAWSLGD FGGSVQDAARAPAE EGGVRASALALFVFLGLPFAVLCSVPFAVTAQLTASRG 434

Query: 460 GGQGLCTGVLNISI VIPQVIIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXXPK 519  
 GGQGLCTGVLNISI V+PQ+ IALGAGPWD LFG+GNIP PK  
 Sbjct: 435 GGQGLCTGVLNISI VVPQMAIALGAGPWDELFGEGNIPAFAMASVFAAAAAAGVLLPK 494

Query: 520 ISKRQFRAVSAGGH 533  
 +S R AGGH  
 Sbjct: 495 VSVRSVSM--AGGH 506

☐ >gi|15718401|dbj|BAB68368.1| sucrose transporter [Oryza sativa (japonica cultiva  
 Length = 506

Score = 586 bits (1511), Expect = e-166  
 Identities = 332/494 (67%), Positives = 376/494 (76%), Gaps = 11/494 (2%)

Query: 43 ISLGRILLAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSMWLCGPIAGLVVQPLVG 102  
 ISL L LA MVAGGVQYGWALQLSLLTPYVQTLG+ HALTS MWLCGPIAGL+VQP VG  
 Sbjct: 21 ISLSGLFLACMVAGGVQYGWALQLSLLTPYVQTLGIPHALTSVMWLCGPIAGLIVQPCVG 80

Query: 103 LYSDRCTSRWGRRRPFILTCMLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHA AI 162  
 LYSD+CTS GRRRPFILTCG++IC++VIV+GFSSDIG ALGDT E C +Y GPR+HAA  
 Sbjct: 81 LYSDKCTSSLGRRRPFILTCGIIICISVIVIGFSSDIGYALGDTTDEDCKVYRGPRYHAAA 140

Query: 163 VYVLGFWLLDFSNNTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNW 222  
 ++LGFWLLDFSNNTVQGPARA+MADL HGPSAAN+IFCSWMALGNILGYSSGSTN+W  
 Sbjct: 141 AFILGFWLLDFSNNTVQGPALMADLSGRHGPSAANAIFCSWMALGNILGYSSGSTNDW 200

Query: 223 HKWFPFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGE 282  
 HKWFPFL T ACCEACANLK +FA+EV L A  
 Sbjct: 201 HKWFPFLMTRACCEACANLKAFLVAVVFLGLSTAVTMVFAREVA-----LDPVAAAKR 254

Query: 283 VETEPTGPLAVLKGFKDLPPGMPSVLLVTAITWLSWFPFIFYDWDWMGREIYHGDPKGSN 342  
 E E +G LAV KG K+LP GMPSVL+VT +TWLSWFPFIL+DTDWMGREIYHG P GS  
 Sbjct: 255 NEGEASGLLAVFKGMKNLPVGMPSVLIVTGLTWLSWFPFILFDTDWMGREIYHGRPDGSP 314

Query: 343 AQISAFNEGVRVGAFGLLLNSVILGFSSFLIEPMCCKVGPVVVWTSNFMVCVAMAATAL 402  
 A+++AF EGVR GAFGLLLNS++LG SSFLIEPMC++G R VWV S+ +VCVAMAA ++  
 Sbjct: 315 AEVTAFAQEGVRQGAFLGLLLNSIVLGISSFLIEPMCRRLGARAVVWMSSAVVCVMAAAVSV 374

Query: 403 ISFWSLRDYGHYVQDAITANAS---IKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRG 459  
 +S WSL D+ G VQDA A A ++A L LF FLG+P A+L SVPFAVTAQLAA+RG  
 Sbjct: 375 LSAWSLGDGFGSVQDAARAPAEEGVRSALALFVFLGLPFAVLCSVPFAVTAQLAASRG 434

Query: 460 GGQGLCTGVLNISIVIPQVIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXPK 519  
 GGQGLCTGVLNISIV+PQ+ IALGAGPWD LFG+GNIP PK  
 Sbjct: 435 GGQGLCTGVLNISIVPQMAIALGAGPWDELFGGNIPAFAMASVFAAAAAAGVLLPK 494

Query: 520 ISKRQFRAVSAGGH 533  
 +S R AGGH  
 Sbjct: 495 VSVRSVSM--AGGH 506

☐ >gi|21063927|gb|AAM29153.1| sucrose transporter 2 [Citrus sinensis]  
 Length = 607

Score = 526 bits (1356), Expect = e-148  
 Identities = 286/559 (51%), Positives = 359/559 (64%), Gaps = 54/559 (9%)

Query: 27 APISLGRILLAGMVAPISLGRILLAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSM 86  
 +PI G A SL L+L+ VA GVQ+GWALQLSLLTPY+QTLG+ HA +SF+  
 Sbjct: 49 SPIPNGTSNFAVRPKQCSLITLVLSCTVAAGVQFGWALQLSLLTPYIQTGLIQHAFSSFI 108

Query: 87 WLCGPIAGLVVQPLVGLYSDRCTSRWGRRRPFILTCMLICVAVIVVGFSSDIGAALGDT 146  
 WLCGPI GLVVQP VG++SD+CTS++GRRRPFIL GC++I VAVI++GFS+DIG LGDT  
 Sbjct: 109 WLCGPITGLVVQPCVGIEWSKCTSKYGRRRPFILAGCLMISVAVIIIGFSADIGYILGDT 168

Query: 147 KEHCSLYHGPRWHA AIVYVLGFWLLDFSNNTVQGPARAMMADLCDHHGPSAANSIFCSWM 206  
 KEHCS + G R AA V+V+GFWLLD +NNTVQGPARA++ADL ++AN+I CSWM  
 Sbjct: 169 KEHCSKFRGTRTRAAFFVFIGFWLLDLNNTVQGPALLADLSGPDQRNSANAILCSWM 228

Query: 207 ALGNILGYSSGSTNNWHKWFPFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXXXXIFAKEV 266  
 A+GNILG+S+G++ +WH+WFPFL + ACC AC NLK FA EV  
 Sbjct: 229 AVGNILGFSAGASGSWHRWFPFLTSRACCAACGNLKAFLVAVVFLTLCALVTIYFADEV 288

Query: 267 PYRANE-----NLPT--TKAGGEVET----- 285  
 P N+ ++P G +VE+  
 Sbjct: 289 PLTVNQPNHLTDSAPLLDDPQRTAISKSKHDMPAAPNANGNKVESGHERDANLKHISKKA 348

Query: 286 -EPT-----GPLAV----LKGFKDLPPGMPSVLLVTAITWLSWFPFIFYDWDWMGREIYH 335  
 +P GP AV L + LPP M VL+V A+TWLSWFPF L+DTDWMGRE+YH  
 Sbjct: 349 EDPNGSFNDGPGAVLVNLLTSLRHLPPAMHVVLVVMALTWLSWFPFFLFDTDWMGREVYH 408

Query: 336 GDPKGSNAQISAFNEGVRVGAFGLLLNSVILGFSSFLIEPMCRKVGPRVWVTSNFMVCV 395  
 GDPKG++ ++ +++GVR GAFGLLLNSV+LG SSFLIEPMCR +G R+VW SNF+V  
 Sbjct: 409 GDPKGNDEHKFYDQGVREGAFGLLLNSVVLGVSSFLIEPMCRWIGSRLVWAI SNFVFA 468

Query: 396 AMAATALISFWSL-RDYHGYVQDAITANASIKAVCLVLFAFLGVPLAILYSVPFAVTAQL 454  
 MA TA+IS S+ R+ ++ I AN +IK LV+F LG PLAI YSVPFA+T +L  
 Sbjct: 469 CMATTAIISVISVRRNILEGIEHGIGANQAIVASLVVFTLLGFPLAITYSVPFAITGEL 528

Query: 455 AATRGGGQGLCTGVLNISIVIPQVIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXX 514  
 A GGGQGL GVLN++IVIPQ+I++LGAGPWDALFG GNIP  
 Sbjct: 529 TADSGGGQGLAIGVLNLAIVIPQMIVSLGAGPWDALFGGNNIPAFGLASLSALAGGVVAT 588

Query: 515 XXXPKISKRQFRAVSAGGH 533  
 P +S F S+G H  
 Sbjct: 589 LKPLHLSSNSF--TSSGFH 605

☐ >gi|29467454|dbj|BAC67164.1| sucrose transporter [Oryza sativa (japonica cultivata  
 Length = 595

Score = 526 bits (1355), Expect = e-148

Identities = 267/499 (53%), Positives = 344/499 (68%), Gaps = 48/499 (9%)

Query: 47 RLILAGMVAGGVQYQWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLYSD 106  
 +L+LA MVA GVQ+GWALQLSLLTPY+QTLG+ HA+ SF+WLCGPI G VVQP VG++SD  
 Sbjct: 61 KLVLACMVAAGVQFGWALQLSLLTPYIQTGLIDHAMASFIWLCGPITGFVVQPCVGVWSD 120

Query: 107 RCTSRWGRRRPFILTGCMILCVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVL 166  
 +C S++GRRRPFIL GC++IC AV ++GFS+D+G LGDT EHCS Y G R+ AAI++VL  
 Sbjct: 121 KCRSKYGRRRPFILAGCLMICFAVTLIGFSADLGYILGDTTEHCSTYKGSRFRAAIIIFVL 180

Query: 167 GFWLLDFSNNTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWF 226  
 GFW+LD +N+TVQGPARA++ADL ++AN+IFC+WMA+GN+LG+SSG++ NWHKWF  
 Sbjct: 181 GFWMLDLANHTVQGPARALLADLSGPDQCNSANAIFCTWMAVGNVLGFSSGASGNWHKWF 240

Query: 227 PFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXXXXIFAKEVPYR----- 269  
 PFL T ACCEAC+NLK FA+E+P  
 Sbjct: 241 PFLMTRACCEACSNLKAFLVAVVFLFCMSVTLYFAEEIPLPTDAQRLSDSAPLLNGS 300

Query: 270 -----ANENLPTTKAGGE-VETEPTGPLAV----LKGFK 298  
 AN N + + E VE GP AV L +  
 Sbjct: 301 RDDNNASNEPRNGALPNGHTDGSNVPANSNAEDSNSNRENVEVFNDGPGAVLVNILTSMR 360

Query: 299 DLPPGMPSVLLVTAITWLSWFPFILIYDTDWMGREIYHGDPKGSNAQISAFNEGVRVGAFG 358  
 LPPGM SVLLV A+TWLSWFPF L+DTDWMGRE+YHGD G+ ++ A++ GVR GAFG  
 Sbjct: 361 HLPPGMYSVLLVMALTWLSWFPFLLFDTDWMGREVYHGD PNGNLSEKAYDNGVREGAFG 420

Query: 359 LLLNSVILGFSSFLIEPMCRKVGPRVWVTSNFMVCVAMAATALISFWSLRDYHGYVQDA 418  
 LLLNSV+LGF SFL++P+CR +G R+VW SNF V + M ATA++S+ S Y +  
 Sbjct: 421 LLLNSVVLGFSGFLVDPLCRLMGARLVWAI SNFTVFICMLATAILSWISFDLYSSKLHHI 480

Query: 419 ITANASIKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQV 478  
 I AN ++K L++F+ LG+PL+I Y VPF+VTA+L A G GQGL TGVLN++IV+PQ+  
 Sbjct: 481 IGANKTVKNSALIVFSLGLPLSITYGVPF SVTAELTAGTGSGQGLATGVLNLAIVVPQI 540

Query: 479 IIALGAGPWDALFGKGNIP 497  
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 Sbjct: 541 VVSLGAGPWDALFGGNNVP 559

☐ >gi|10119908|gb|AAG12987.1|AF166498.1 sucrose transporter-like protein [Lycopers  
 Length = 604

Score = 525 bits (1353), Expect = e-148

Identities = 269/508 (52%), Positives = 336/508 (66%), Gaps = 54/508 (10%)

Query: 44 SLGRLILAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGL 103  
SL LIL+ VA GVQ+GWALQLSLLTPY+QTLG+ HA +SF+WLCGPI GLVVQP VG+

Sbjct: 62 SLLTLILSCTVAAGVQFGWALQLSLLTPYIQTGLGIEHAFSSFIWLCGPITGLVVQPCVGI 121

Query: 104 YSDRCTSRWGRRRPFILTGCMCLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIV 163  
+SD+C S++GRRRPFI G ++I +AVI++GFS+DIG LGDTKEHCS + G R AAIV

Sbjct: 122 WSDKCHSKYGRRRPFIFIGAVMISIAVIIIGFSADIGYLLGDTKEHCSTFKGTRSRAAIV 181

Query: 164 YVLGFWLLDFSNNTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWH 223  
+V+GFW+LD +NNTVQGPARGA++ADL + AN++FCSWMA+GNILG+S+G++ WH

Sbjct: 182 FVVGFWMLDLANNTVQGPARGALLADLSGPDQRNTANAVFCSWMAVGNILGFSAGASGGWH 241

Query: 224 KWFPFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXXXXXIFAKEVP----- 267  
+WFPFL ACCE C NLK FA EVP

Sbjct: 242 RWFPFLTNACCEPCGNLKAFLVAVVFLTLCTLVTLTYFANEVPLSPKQYKRMSDSAPLL 301

Query: 268 -----YRAN-----ENLPTTKAGGEVETEPTGP 290  
YR + E P G P

Sbjct: 302 DSPQNTGFDLQSRELQYRNSVANNESEMGHVADNSPKNEEQRPDKDQGDSFADSPGAV 361

Query: 291 LA-VLKGFKDLPPGMPSVLLVTAITWLSWFPFIFYDTDWMGREIYHGDPKGSNAQISAFN 349  
L +L + LPP M SVL+V A+TWLSWFPF L+DTDWMGRE+YHGDPKG +++A+N

Sbjct: 362 LVNLLTSLRHLPPAMHSVLIVMALTWLSWFPFFLFDTDWMGREVYHGDPKGEADEVNAYN 421

Query: 350 EGV RVGAFGLLLNSVILGFSSFLIEPMCCKRVGPRVWVTSNFMVCVAMAATALISFWSLR 409  
+GVR GAFGLLLNSV+LG SSFLIEPMC+ +G R+VW SNF+V V MA TA+IS S+

Sbjct: 422 QGVREGAFGLLLNSVVLGVSSFLIEPMCCKWIGSRLVWAVSNFVFCMACTAISVVSIS 481

Query: 410 DYHGYVQDAITANASIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVL 469  
VQ I A S + LV+F+ LG+PLA+ YSVPF++TA+L A GGGQGL GVL

Sbjct: 482 ANTQGVQHVIGATRSTQIAALVVFSLLGIPLAVTYSVPFSITAELTADAGGGQGLAIGVL 541

Query: 470 NISIVIPQVIIALGAGPWDALFGKGNIP 497  
N++IV+PQ++++LGAGPWDALFG GNIP

Sbjct: 542 NLAIVVPQMVSLLGAGPWDALFGGGNIP 569

☐ >gi|15227049|ref|NP\_178389.1| putative sucrose/H+ symporter; protein id: At2g028  
thaliana]

gi|25344715|pir|G84441 probable sucrose-proton symporter [imported] - Arabidopsi

gi|3461813|gb|AAC32907.1| putative sucrose/H+ symporter [Arabidopsis thaliana]

gi|8052190|emb|CAB92307.1| sucrose transporter [Arabidopsis thaliana]

Length = 594

Score = 523 bits (1348), Expect = e-147

Identities = 261/501 (52%), Positives = 336/501 (67%), Gaps = 47/501 (9%)

Query: 44 SLGRLILAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGL 103  
SL L+L+ VA GVQ+GWALQLSLLTPY+QTLG+SHA +SF+WLCGPI GLVVQP VG+

Sbjct: 59 SLVTLVLSCTVAAGVQFGWALQLSLLTPYIQTGLGISHAFSSFIWLCGPITGLVVQPFVGI 118

Query: 104 YSDRCTSRWGRRRPFILTGCMCLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIV 163  
+SD+CTS++GRRRPFIL G +I +AVI++GFS+DIG LGD+KEHCS + G R AA+V

Sbjct: 119 WSDKCTSKYGRRRPFILVGSFMISIAVIIIGFSADIGYLLGDSKEHCSTFKGTRTRAADV 178

Query: 164 YVLGFWLLDFSNNTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWH 223  
+++GFWLLD +NNTVQGPARGA++ADL + AN++FC WMA+GNILG+S+G++ W

Sbjct: 179 FIIGFWLLDLANNTVQGPARGALLADLSGPDQRNTANAVFCLWMAIGNILGFSAGASGKWQ 238

Query: 224 KWFPFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXXXXXIFAKEVPYRAN----- 271  
+WFPFL + ACC AC NLK FAKE+P+ +N

Sbjct: 239 EWFPFLTSRACCAACGNLKAFLVAVVFLTICTLVTLTYFAKEIPFTSNKPTRIQDSAPLL 298

Query: 272 -----ENLPTTKAGGEVETEPTGPLAV-----LKG 296  
E ++ + ET GP +V L

Sbjct: 299 DDLQSKGLEHSLNNGTANGIKYERVERDTEQFGNSENEHQDETYVDGPGSVLVNLLTS 358

Query: 297 FKDLPPGMPSVLLVTAITWLSWFPFIFYD TDWMGREIYHGDPKGSNAQISAFNEGVRVGA 356  
 + LPP M SVL+V A+TWLSWFPF L+DTDWMGRE+YHGDP G + + +++GVR GA  
 Sbjct: 359 LRHLPPAMHSVLIVMALTWLSWFPFFLFD TDWMGREVYHGDP TGD SLHME LYDQGVREGA 418

Query: 357 FGLLLNSVILGFSSFLIEPMC RKVGPRVWVTSNFMVCVAMAATALISFWSLRDYHGYVQ 416  
 GLLLSNV+LG SSFLIEPMC+++G RVVW SNF V MA TA+IS SL D ++  
 Sbjct: 419 LGLLLNSVVLGISSFLIEPMCQRMGARVVWALS NF TVFACMAGTAVISLMSLSDDKNGIE 478

Query: 417 DAITANASIKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVNLISIVIP 476  
 + N + + +++FA LG PLAI YSVPF+VTA++ A GGGQGL GVLN++IVIP  
 Sbjct: 479 YIMRGNETTRTAAVIVFALLGFPLAITYSVPFSVTA EVTADSGGGQGLAIGVLNLAIVIP 538

Query: 477 QVIIALGAGPWDALFGKGNIP 497  
 Q+I++LGAGPWD LFG GN+P  
 Sbjct: 539 QMIVSLGAGPWDQLFGGNNLP 559

☐ >gi|6434831|gb|AAF08330.1|AF021809 1 putative sucrose transporter [Vitis vinifer]  
 Length = 612

Score = 517 bits (1331), Expect = e-145  
 Identities = 272/507 (53%), Positives = 340/507 (67%), Gaps = 54/507 (10%)

Query: 45 LGRLLLAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLY 104  
 L LIL+ M+A GVQ+GWALQLSLLTPY+QTLG+ HA +SF+WLCGPI GLVVQP VG++  
 Sbjct: 63 LRTLILSCMIAAGVQFGWALQLSLLTPYIQTLGIEHAFSSFIWLCGPITGLVVQPCVGIW 122

Query: 105 SDRCTSRWGRRRPFILTGCM LICVAVIVGFSSDIGAALGDTKEHCSLYHGPRWHA AIVY 164  
 SD+C+S++GRRRPFIL G ++I VAV ++GFS+DIG LGDT C + G R AAI++  
 Sbjct: 123 SDKCSSKYGRRRPFILAGSLMISVAVTIIGFSADIGYLLGDTNMDCRKFKGTRTWAAIIF 182

Query: 165 VLGFWLLDFSNN TVQGPARAMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHK 224  
 VLGFW+LD +NNTVQGPARA++ADL ++AN+IFCSWMA+GNILG+S+G++ +WH+  
 Sbjct: 183 VLGFWM LLDANNTVQGPARALLADLSGPDQRNSANAIFCSWMAVGNILGFSAGASGHWHR 242

Query: 225 WFPFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXIFAKEVP----- 267  
 WFPFL ACCEAC NLK FA+EVP  
 Sbjct: 243 WFPFLNLKACCEACGNLKA AFLIAVFLTLCTLVTLYFAEEVPLMAYQPHHLSDSAPLLD 302

Query: 268 -----YRANENLP--TTKAGGEVETEPTGPLAV-- 293  
 Y N+N T + E+ GP AV  
 Sbjct: 303 NPQQIGFDNSKSKLDMSAVDNATGNNPESSYEINKNAKHLTPIVQE QNESFSDGPGAVLV 362

Query: 294 --LKGFKDLPPGMPSVLLVTAITWLSWFPFIFYD TDWMGREIYHGDPKGSNAQISAFNEG 351  
 L + LPP M SVLLV A++WLSWFPF L+DTDWMGRE+YHGDPKG + + A++ G  
 Sbjct: 363 NLLTSLRHLPPAMHSVLLVMALSWLSWFPFFLFD TDWMGREVYHGDPKGDES AVKAYDAG 422

Query: 352 VRVGAFGLLLNSVILGFSSFLIEPMC RKVGPRVWVTSNFMVCVAMAATALISFWSLRDY 411  
 VR GAFGLLLNSV LG SSFLIEPMC+++G R+VW SNF+V MA TA+IS S+ +Y  
 Sbjct: 423 VREGAFGLLLNSVDLGISSFLIEPMCQRMGARLVWAMSNFIVFACMAGTAIISLVS VNEY 482

Query: 412 HGY-VQDAITANASIKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVNL 470  
 +Q AI N +IK LV+FA LG PL+I YSVPF++TA+L A GGGQGL GVLN  
 Sbjct: 483 ITEGIQHAIGENRAIKIASLVVFALLGFPLSITYSVPF SITAE LTADTGGGQGLAIGVLN 542

Query: 471 ISIVIPQVIIALGAGPWDALFGKGNIP 497  
 ++IVIPQ+I++LGAGPWDALFG GNIP  
 Sbjct: 543 LAIVIPQMIVSLGAGPWDALFGGNNIP 569

☐ >gi|29467456|dbj|BAC67165.1| sucrose transporter [Oryza sativa (japonica cultivar)]  
 Length = 535

Score = 502 bits (1293), Expect = e-141  
 Identities = 261/489 (53%), Positives = 333/489 (68%), Gaps = 8/489 (1%)



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RPS-BLAST 2.2.5 [Nov-16-2002]

Query= local sequence:  
(533 letters)Database: cdd.v1.61  
10,927 PSSMs; 2,688,589 total columns

Click on boxes for multiple alignments

 Domain RelativesPSSMs producing significant alignments: Score E  
(bits) value[gnl|CDD|11918](#) COG2211, MelB, Na<sup>+</sup>/melibiose symporter and related transporter... 47.9 3e-06

---

[gnl|CDD|11918](#), COG2211, MelB, Na<sup>+</sup>/melibiose symporter and related transporters [Carbohydrate transport and metabolism]CD-Length = 467 residues, only 26.3% aligned  
Score = 47.9 bits (114), Expect = 3e-06

Query:	42	PISLGRILLAGM--VAGGVQYGWALQLSLTPYVQTLGLSHALTSFMWLCGPIAGLVVQP	99
Sbjct:	8	KLSLKEKIGYGLGDFASNFAFG-IVVLYLLFFYTDVFGLSAALAGTIFLVARIIDAITDP	66
Query:	100	LVGLYSDRCTSRWGRRRPFILTGCM LICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWH	159
Sbjct:	67	IMGFIVDRTRSRWGRFRPWLLWGAIPFAIVAVLLFITPDFS-----MTGKLIY	114
Query:	160	AAIVYVLGFWLLDFSN	175
Sbjct:	115	ALVTYMLLGLGYTLVN	130

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RPS-BLAST 2.2.5 [Nov-16-2002]

Query= local sequence:  
(533 letters)Database: cdd.v1.61  
10,927 PSSMs; 2,688,589 total columns

Click on boxes for multiple alignments

[Show](#) Domain RelativesPSSMs producing significant alignments: Score E  
(bits) value[gnl|CDD|11918](#) COG2211, MelB, Na<sup>+</sup>/melibiose symporter and related transporter... 47.9 3e-06

---

[gnl|CDD|11918](#), COG2211, MelB, Na<sup>+</sup>/melibiose symporter and related transporters [Carbohydrate transport and metabolism]CD-Length = 467 residues, only 26.3% aligned  
Score = 47.9 bits (114), Expect = 3e-06

Query:	42	PISLGRILLAGM--VAGGVQYGWALQLSLTPYVQTLGLSHALTSFMWLCGPIAGLVVQP	99
Sbjct:	8	KLSLKEKIGYGLGDFASNFAFG-IVVLYLLFFYTDVFGLSAALAGTIFLVARIIDAIDTP	66
Query:	100	LVGLYSDRCTSRWGRRRPFILTGCM LICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWH	159
Sbjct:	67	IMGFIVDRTRSRWGRFRPWLLWGAIPFAIVAVLLFITPDFS-----MTGKLIY	114
Query:	160	AAIVYVLGFWLLDFSN	175
Sbjct:	115	ALVTYMLLGLGYTLVN	130

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PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books
Search	Protein	▼ for					Go	Clear
		Limits	Preview/Index	History	Clipboard		Details	
Display	default	▼ Show: 20	▼ Send to	File	▼ Get Subsequence			

☐ 1: AAF90181. sucrose transport...[gi:9624451]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAF90181 538 aa linear PLN 07-APR-2003  
 DEFINITION sucrose transporter [Oryza sativa (indica cultivar-group)].  
 ACCESSION AAF90181  
 VERSION AAF90181.1 GI:9624451  
 DBSOURCE accession AF280050.1  
 KEYWORDS  
 SOURCE Oryza sativa (indica cultivar-group)  
 ORGANISM Oryza sativa (indica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 REFERENCE 1 (residues 1 to 538)  
 AUTHORS Aoki,N., Hirose,T., Scofield,G.N., Whitfeld,P.R. and Furbank,R.T.  
 TITLE The sucrose transporter gene family in rice  
 JOURNAL Plant Cell Physiol. 44 (3), 223-232 (2003)  
 MEDLINE 22555500  
 PUBMED 12668768  
 REFERENCE 2 (residues 1 to 538)  
 AUTHORS Whitfeld,P.R. and Furbank,R.T.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-JUN-2000) CSIRO Plant Industry, GPO Box 1600,  
 Canberra, ACT 2601, Australia  
 COMMENT Method: conceptual translation supplied by author.  
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 AF280050.1:5674..5749,AF280050.1:5975..6169,  
 AF280050.1:6288..6431,AF280050.1:6541..6774,  
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#### ORIGIN

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241 eacanlkgaf lvavifslc lvitlifake vpfkgnaalp tksnepaepe gtgplavlkq
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PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books
Search		Protein	for		Go		Clear	
Limits		Preview/Index		History		Clipboard		Details
Display	default	Show:	20	Send to	File	Get Subsequence		

☐ 1: AAF90181. sucrose transport...[gi:9624451][BLink](#), [Domains](#), [Links](#)

LOCUS AAF90181 538 aa linear PLN 07-APR-2003  
DEFINITION sucrose transporter [Oryza sativa (indica cultivar-group)].  
ACCESSION AAF90181  
VERSION AAF90181.1 GI:9624451  
DBSOURCE accession AF280050.1  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (residues 1 to 538)  
AUTHORS Aoki,N., Hirose,T., Scofield,G.N., Whitfeld,P.R. and Furbank,R.T.  
TITLE The sucrose transporter gene family in rice  
JOURNAL Plant Cell Physiol. 44 (3), 223-232 (2003)  
MEDLINE 22555500  
PUBMED 12668768  
REFERENCE 2 (residues 1 to 538)  
AUTHORS Whitfeld,P.R. and Furbank,R.T.  
TITLE Direct Submission  
JOURNAL Submitted (19-JUN-2000) CSIRO Plant Industry, GPO Box 1600,  
Canberra, ACT 2601, Australia  
COMMENT Method: conceptual translation supplied by author.  
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## ORIGIN

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421 kaitadksik avclvlfafl gvplavlysv pfavtaqlaa trggggglct gvlnisivip
481 qvvialgagp wdelfgkgni pafglasgfa liggvagifl lpkiskrqfr svsmgggh
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PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	MIM	Books
Search		Protein	for				Go	Clear
Limits		Preview/Index		History		Clipboard		Details
Display	default	Show:	20	Send to	File	Get Subsequence		

# ☐ 1: BAA83501. Sucrose Transport...[gi:5771354]

[BLink](#), [Domains](#), [Links](#)

LOCUS BAA83501 521 aa linear PLN 26-AUG-1999  
 DEFINITION Sucrose Transporter [Zea mays].  
 ACCESSION BAA83501  
 VERSION BAA83501.1 GI:5771354  
 DBSOURCE accession [AB008464.1](#)  
 KEYWORDS .  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (sites)

AUTHORS Aoki,N., Hirose,T., Takahashi,S., Ono,K., Ishimaru,K. and Ohsugi,R.  
 TITLE Molecular cloning and expression analysis of a gene for a sucrose  
 transporter in maize (Zea mays L.)  
 JOURNAL Plant Cell Physiol. (1999) In press

REFERENCE 2 (residues 1 to 521)

AUTHORS Aoki,N.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-OCT-1997) Naohiro Aoki, Japan International Research  
 Center for Agricultural Sciences, Biological Resources Division;  
 1-2 Ohwashi, Tsukuba, Ibaraki 305, Japan  
 (E-mail:[naoki@ss.jircas.affrc.go.jp](mailto:naoki@ss.jircas.affrc.go.jp), Tel:81-0298-38-6305,  
 Fax:81-0298-38-6650)

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## ORIGIN

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121 vvgfssdiga  algdtkehcs  lyhgprwhaa  ivyvlgfll  dfsnntvqgp  arammadlcg
181 hhgpsaansi  fcswmalgni  lgyssgstnn  whkwfpfllt  nacceacanl  kgaf1vavvf
241 lvmcltv1tf  fanevpyrgn  qnlptkange  vetepsgpla  vlkgfkn1pt  gmpsvllvtg
301 ltwlswfpfi  lytdwmgre  iyhgdpkgsn  aqisafdegv  rvgsfgllln  sivlgfssfl
361 iepmcrkvqp  rvvwtsnfm  vcvamaatal  isfws1kdyh  gyvqda1tas  tsikavclvl
421 faflgvplai  lysvpfavta  qlaatkgggg  glctgvlnis  ivipqviial  gagpwdal1g
481 kgnipafgva  sgfaliggvv  gvfl1pkisk  rqfravsagg  h

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